AUG 0 4 2006
PATENT & TRADEMARK OFFICE

I HEREBY CERTIFY THAT THIS CORRESPONDENCE IS BEING DEPOSITED WITH THE UNITED STATES POSTAL SERVICE AS FIRST CLASS MAIL IN AN ENVELOPE ADDRESSED TO: COMMISSIONER FOR PATENTS, P.O. BOX 1450, ALEXANDRIA, VA 22313-1450, ON THE DATE INDICATED BELOW.

BY: _____ Date: August 1, 2006

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

First Named Inventor:	Nobuya ITOH	§	Group Art Unit: 1652
		§	
		§	
Conf. No.:	7835	§	Examiner: Kagnew H. Gebreyesus, Ph.D.
		§	
Appln. No.:	10/782,998	§	Allowed May 2, 2006
		§	
Filing Date:	February 20, 2004	§	Attorney Docket No.: 600630-15US
		§	(562737)

Title: REDUCTASE GENE AND USE OF THE SAME

DECLARATION OF HIROYUKI ASAKO
REGARDING SECOND REPLACEMENT SEQUENCE LISTINGS

I, Hiroyuki Asako, hereby declare as follows:

1. I am the research associate with Sumitomo Chemical Co., Ltd. ("Sumitomo"), the assignee of the rights in the above-identified patent application, based on an Assignment from the inventor, Nobuya Itoh, recorded in the U.S. Patent and Trademark Office on April 21, 2004, at Reel 015247, beginning at Frame 0239. I graduated with a Masters Degree from Tokyo Institute of Technology Department of Bioscience and Biotechnology in March, 1997. I began at Sumitomo in April, 1997 and have been engaged in biochemical research such as gene technology, fermentation, recombinant technology, bioconversion, and the like. I have been working with the inventor and Sumitomo's patent attorneys and am familiar with this application and its file history.

2. I was asked to review the application following receipt of the second Notice of Allowance dated May 2, 2006, prior to payment of the issue fee to make sure that the information in the application is accurate. Upon reviewing the Amended Sequence Listing filed

March 13, 2006, I realized that further corrections to the Sequence Listings for SEQ ID NOS:1 and 2 are needed.

3. The errors occurred as a result of yet further simple mistakes when reading the nucleotide sequence of SEQ ID NO:2 of the original gene of plasmid ptrTFAR that was analyzed with an ABI Prism 310 Genetic Analyzer, where the mistakes are identified as follows:

(1) 123rd Nucleotide (123rd Original Nucleotide): Peak of "C" was buried by peak "A" due to succession of "A".

(2) 246th Nucleotide (246th Original Nucleotide): Peak of "C" was confirmed by performing analysis again. Same as original sequence.

(Correction made in the 1st Declaration turned out to be wrong)

(3) 467th Nucleotide (467th Original Nucleotide): Peak of "C" was buried by peak "G" due to continuation of "G" and "C".

(4) 575th Nucleotide (between 574th and 575th Original Nucleotide): Peak of "C" was buried due to continuation of "C" and low sensitivity of peak "C".

(5) 590th Nucleotide (between 588th and 589th Original Nucleotide): Peak of "C" was buried due to succession of "G" and "C" and low sensitivity of peak "C".

(6) 595th Nucleotide (593rd Original Nucleotide): Peak of "C" was buried due to succession of "T" and "C" and low sensitivity of peak "C".

(7) 597th Nucleotide (595th Original Nucleotide): Peak of "C" was buried due to succession of "T" and "C" and low sensitivity of peak "C".

(8) 619th Nucleotide (617th Original Nucleotide): Peak of "C" was buried by peak "T" due to continuation of "T" and "C".

(9) 622nd Nucleotide (620th Original Nucleotide): Peak of "G" was buried due to succession of "A" and "G" and low sensitivity of peak "G".

(10) 627th Nucleotide (between 624th and 625th Original Nucleotide): Peak of "C" was confirmed by performing analysis again.

(11) 695th Nucleotide (692nd Original Nucleotide): Peak of "A" was confirmed by performing analysis again. Same as original sequence.

(Correction made in the 1st Declaration turned out to be wrong)

4. Attached is a copy of a ClustalW Formatted Alignments printout showing the nine mistakes identified in paragraph 3 above. Also attached is a comparison of the original and amended nucleotide sequence for SEQ ID NO:1, based on the corrections to the nucleotide sequence of SEQ ID NO:2.

5. The errors were inadvertent and without any disceptive intention.

6. Since the DNA of SEQ ID NO:2 is from the same Leifsonia sp. S-749 (Accession No. of International Depositary Authority: FERM BP-8291) and is the original gene of plasmid ptrTFAR as set forth in the application, no new matter has been added by correcting the nucleotide sequence of the DNA in SEQ ID NO:2.

7. In view of the corrections made to SEQ ID NO:2, the corresponding amino acids of SEQ ID NO:1 coded by the DNA of SEQ ID NO:2 also required correction. The corrections are noted in the attached comparison of the original amino acid sequence and the amended amino acid sequence for SEQ ID NO:1. For the same reasons as mentioned in paragraph 6, although corrections have been made to the amino acid sequence, no new matter has been added.

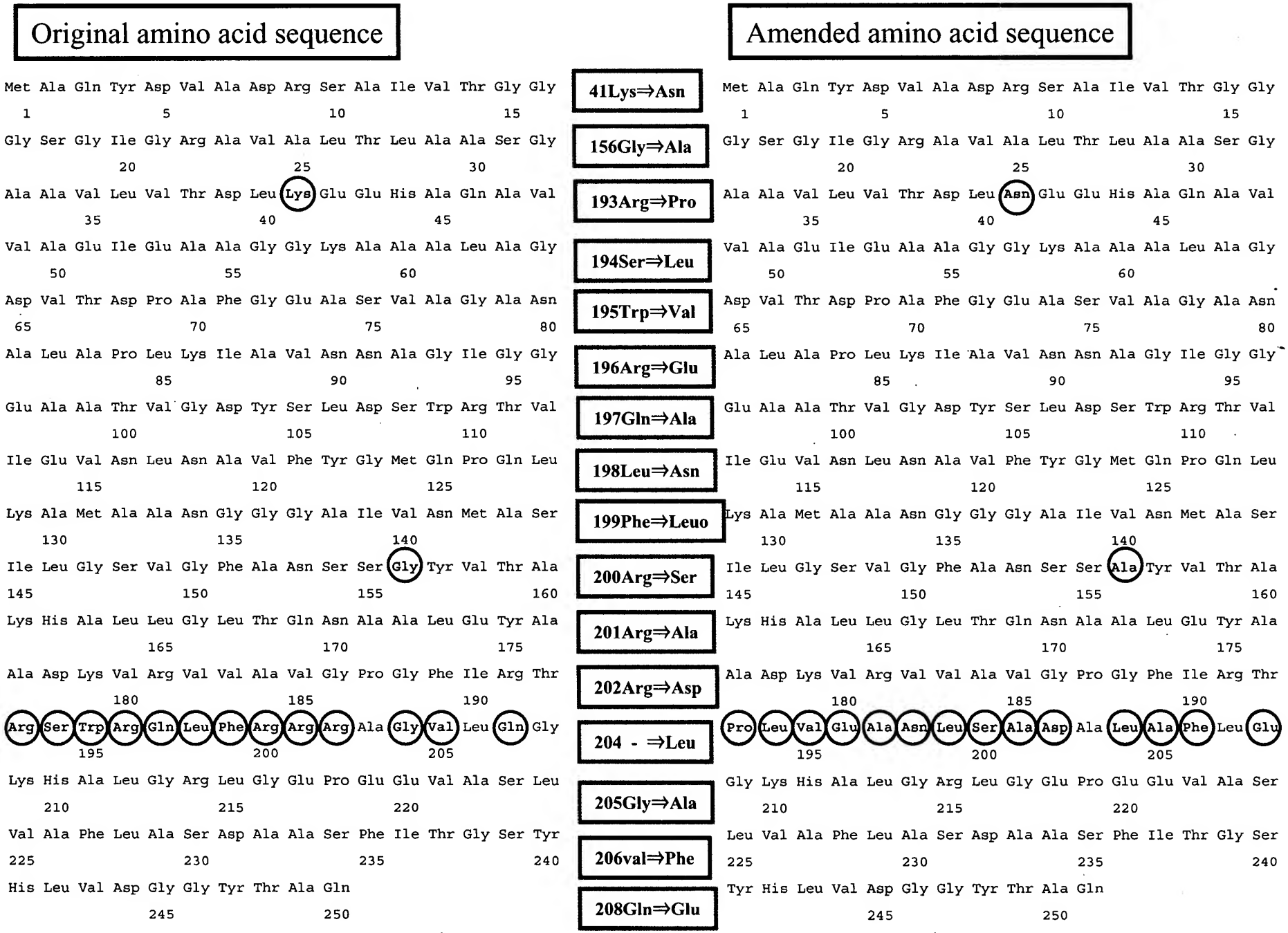
I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

HIROYUKI ASAKO

July 24, 2006 (Date)

Hiroyuki Asako

SEQ ID NO: 1


Original amino acid sequence
Amended amino acid sequence
41Lys⇒Asn
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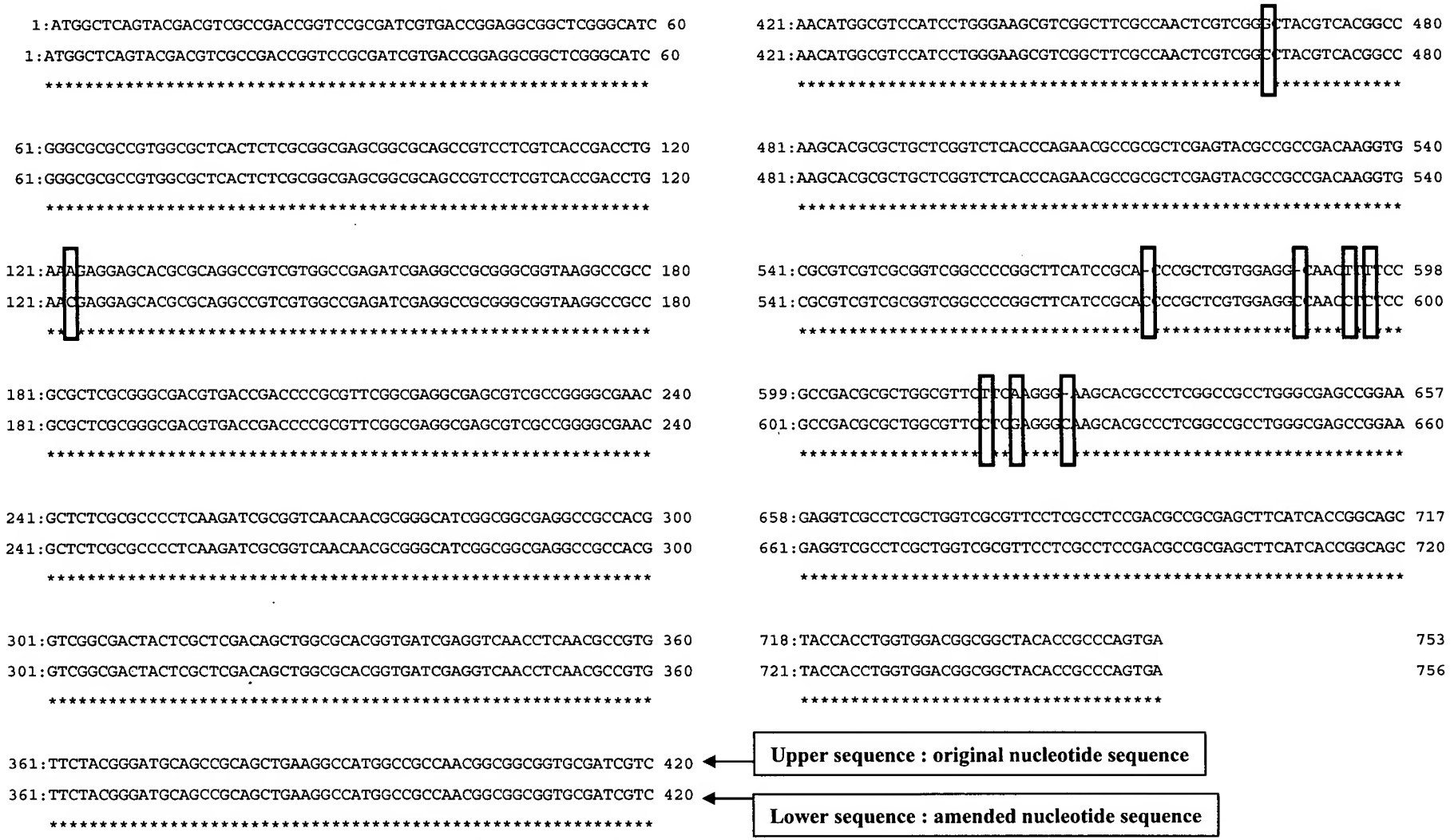
193Arg⇒Pro
194Ser⇒Leu
195Trp⇒Val
196Arg⇒Glu
197Gln⇒Ala
198Leu⇒Asn
199Phe⇒Leuo
200Arg⇒Ser
201Arg⇒Ala
202Arg⇒Asp
204 - ⇒Leu
205Gly⇒Ala
206val⇒Phe
208Gln⇒Glu
Met Ala Gln Tyr Asp Val Ala Asp Arg Ser Ala Ile Val Thr Gly Gly
Gly Ser Gly Ile Gly Arg Ala Val Ala Leu Thr Leu Ala Ala Ser Gly
Ala Ala Val Leu Val Thr Asp Leu Lys Glu Glu His Ala Gln Ala Val
Val Ala Glu Ile Glu Ala Ala Gly Gly Lys Ala Ala Ala Leu Ala Gly
Asp Val Thr Asp Pro Ala Phe Gly Glu Ala Ser Val Ala Gly Ala Asn
Ala Leu Ala Pro Leu Lys Ile Ala Val Asn Asn Ala Gly Ile Gly Gly
Glu Ala Ala Thr Val Gly Asp Tyr Ser Leu Asp Ser Trp Arg Thr Val
Ile Glu Val Asn Leu Asn Ala Val Phe Tyr Gly Met Gln Pro Gln Leu
Lys Ala Met Ala Ala Asn Gly Gly Gly Ala Ile Val Asn Met Ala Ser
Ile Leu Gly Ser Val Gly Phe Ala Asn Ser Ser Gly Tyr Val Thr Ala
Lys His Ala Leu Leu Gly Leu Thr Gln Asn Ala Ala Leu Glu Tyr Ala
Ala Asp Lys Val Arg Val Val Ala Val Gly Pro Gly Phe Ile Arg Thr
Arg Ser Trp Arg Gln Leu Phe Arg Arg Arg Ala Gly Val Leu Gln Gly
Lys His Ala Leu Gly Arg Leu Gly Glu Pro Glu Glu Val Ala Ser Leu
Val Ala Phe Leu Ala Ser Asp Ala Ala Ser Phe Ile Thr Gly Ser Tyr
His Leu Val Asp Gly Gly Tyr Thr Ala Gln
Met Ala Gln Tyr Asp Val Ala Asp Arg Ser Ala Ile Val Thr Gly Gly
Gly Ser Gly Ile Gly Arg Ala Val Ala Leu Thr Leu Ala Ala Ser Gly
Ala Ala Val Leu Val Thr Asp Leu Asn Glu Glu His Ala Gln Ala Val
Val Ala Glu Ile Glu Ala Ala Gly Gly Lys Ala Ala Ala Leu Ala Gly
Asp Val Thr Asp Pro Ala Phe Gly Glu Ala Ser Val Ala Gly Ala Asn
Ala Leu Ala Pro Leu Lys Ile Ala Val Asn Asn Ala Gly Ile Gly Gly
Glu Ala Ala Thr Val Gly Asp Tyr Ser Leu Asp Ser Trp Arg Thr Val
Ile Glu Val Asn Leu Asn Ala Val Phe Tyr Gly Met Gln Pro Gln Leu
Lys Ala Met Ala Ala Asn Gly Gly Gly Ala Ile Val Asn Met Ala Ser
Ile Leu Gly Ser Val Gly Phe Ala Asn Ser Ser Ala Tyr Val Thr Ala
Lys His Ala Leu Leu Gly Leu Thr Gln Asn Ala Ala Leu Glu Tyr Ala
Ala Asp Lys Val Arg Val Val Ala Val Gly Pro Gly Phe Ile Arg Thr
Pro Leu Val Glu Ala Asn Leu Ser Ala Asp Ala Leu Ala Phe Leu Glu
Gly Lys His Ala Leu Gly Arg Leu Gly Glu Pro Glu Glu Val Ala Ser
Leu Val Ala Phe Leu Ala Ser Asp Ala Ala Ser Phe Ile Thr Gly Ser
Tyr His Leu Val Asp Gly Gly Tyr Thr Ala Gln

SEQ ID NO:2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1:ATGGCTCAGTACGACGTCGCCGACCGGTCCGCGATCGTGACCGGAGGCGGCTCGGGCATC 60
421:AACATGGCGTCCATCCTGGGAAGCGTCGGCTTCGCCAACTCGTCGGGCTACGTCACGGCC 480
421:AACATGGCGTCCATCCTGGGAAGCGTCGGCTTCGCCAACTCGTCGGCCTACGTCACGGCC 480
61:GGGCGCGCCGTGGCGCTCACTCTCGCGGCGAGCGGCGCAGCCGTCCTCGTCACCGACCTG 120
61:GGGCGCGCCGTGGCGCTCACTCTCGCGGCGAGCGGCGCAGCCGTCCTCGTCACCGACCTG 120
481:AAGCACGCGCTGCTCGGTCTCACCCAGAACGCCGCGCTCGAGTACGCCGCCGACAAGGTG 540
481:AAGCACGCGCTGCTCGGTCTCACCCAGAACGCCGCGCTCGAGTACGCCGCCGACAAGGTG 540
121:AAAGAGGAGCACGCGCAGGCCGTCGTGGCCGAGATCGAGGCCGCGGGCGGTAAGGCCGCC 180
121:AACGAGGAGCACGCGCAGGCCGTCGTGGCCGAGATCGAGGCCGCGGGCGGTAAGGCCGCC 180
541:CGCGTCGTCGCGGTCGGCCCCGGCTTCATCCGCA-CCCGCTCGTGGAGG-CAACTTTTCC 598
541:CGCGTCGTCGCGGTCGGCCCCGGCTTCATCCGCACCCCGCTCGTGGAGGCCAACCTTTCC 600
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599:GCCGACGCGCTGGCGTTCTTCAAGGG-AAGCACGCCCTCGGCCGCCTGGGCGAGCCGGAA 657
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658:GAGGTCGCCTCGCTGGTCGCGTTCCTCGCCTCCGACGCCGCGAGCTTCATCACCGGCAGC 717
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301:GTCGGCGACTACTCGCTCGACAGCTGGCGCACGGTGATCGAGGTCAACCTCAACGCCGTG 360
718:TACCACCTGGTGGACGGCGGCTACACCGCCCAGTGA 753
721:TACCACCTGGTGGACGGCGGCTACACCGCCCAGTGA 756
361:TTCTACGGGATGCAGCCGCAGCTGAAGGCCATGGCCGCCAACGGCGGCGGTGCGATCGTC 420
361:TTCTACGGGATGCAGCCGCAGCTGAAGGCCATGGCCGCCAACGGCGGCGGTGCGATCGTC 420
Upper sequence : original nucleotide sequence
Lower sequence : amended nucleotide sequence
123A⇒C
467G⇒C
575 - ⇒C
590 -⇒C
595T⇒C
597T⇒C
619T⇒C
622A⇒G
627 -⇒C